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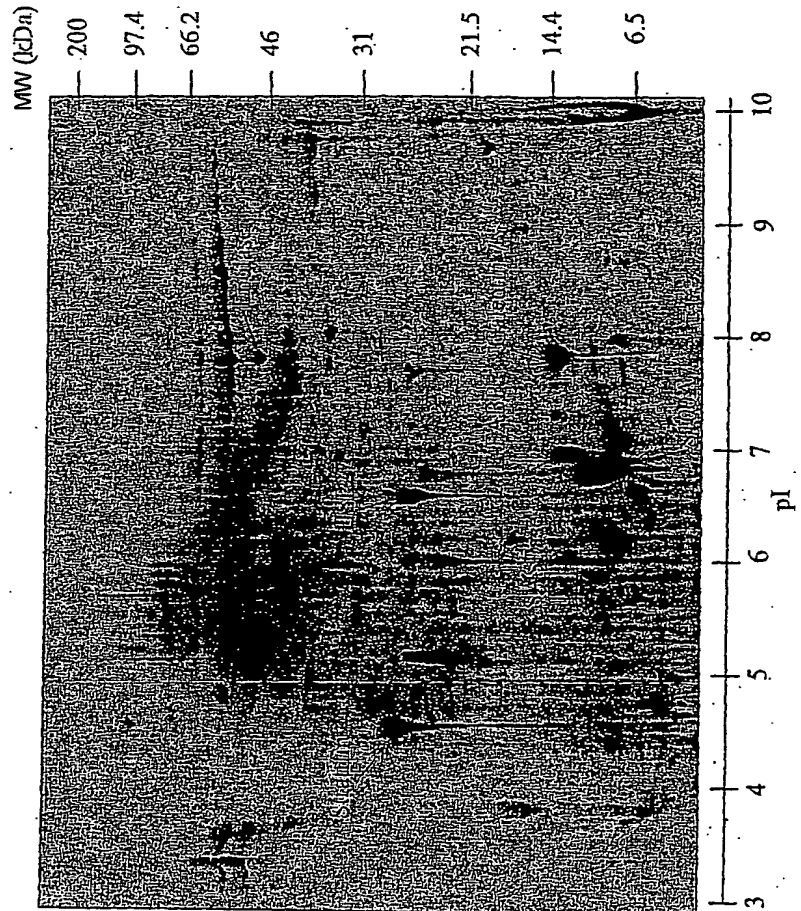


Figure 1

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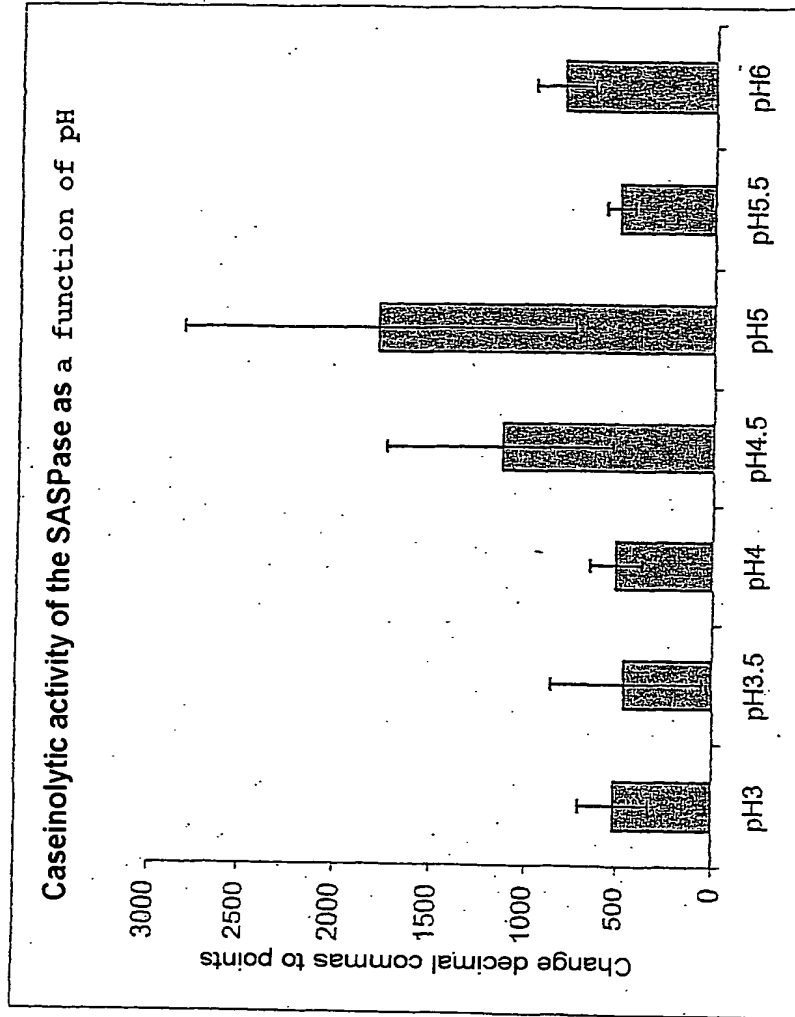


Figure 2

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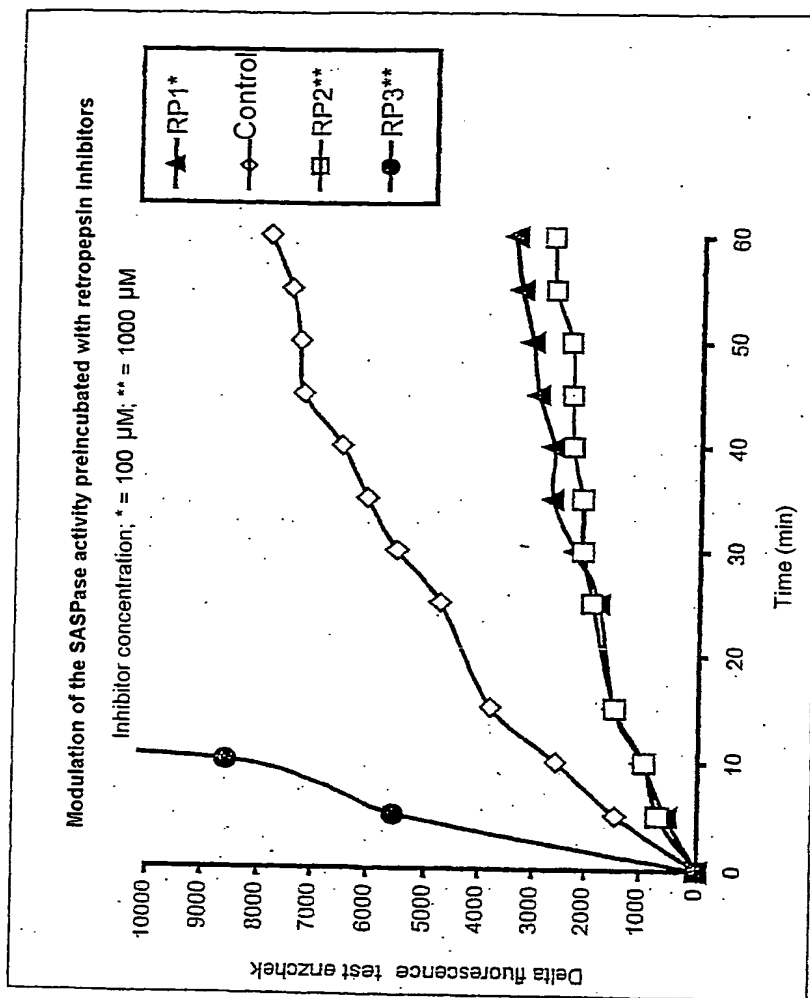


Figure 3

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CLUSTAL W (1.81) multiple sequence alignment

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FIAV      IGFVNYNKGVTGTTTLEKRPETLIFVNGYPIKFLDGTGADITILNRRDFQVKN-----SIE 55
HIV2      -----PQFSLWKRPPVVTAYIEGQPVVEVLDDTGADDSIVAG--IELGN-----NYS 43
SASPase   -----ANSMGKGYYLKGKIGKVPVRFLVDGSAQVSVVHPNLWEEVTDGDLDTLQ 49
           :: * : : * : * : * : * : * : * : * : * : * : * : * : * :
FIAV      NGRQNMIG-VGGGKRGTNYINVHLEIRDENYKTQCIFGNVCVLEDNLSLIQPLIGRDNMK 114
HIV2      ---PKIVGGIGGFINTKEYKNVEIEVLNKKVRATIMTG-----DTPIN-IFGRNLT 92
SASPase   PFENVVKVANGAEMKILGVWDTAVSLGKLKKAQFLVAN-----ASAEAAIIGTDVLQD 103
           : * . . : . : . : . : . : . : . : . : . : . : . : . :
FIAV      FNIRLVMAQ-----123
HIV2      LGMSLNL-----99
SASPase   HNAILDFEHRCTLKGKKFRLLPVGGSLEDEFDLE 138
           . * :

```

Figure 4

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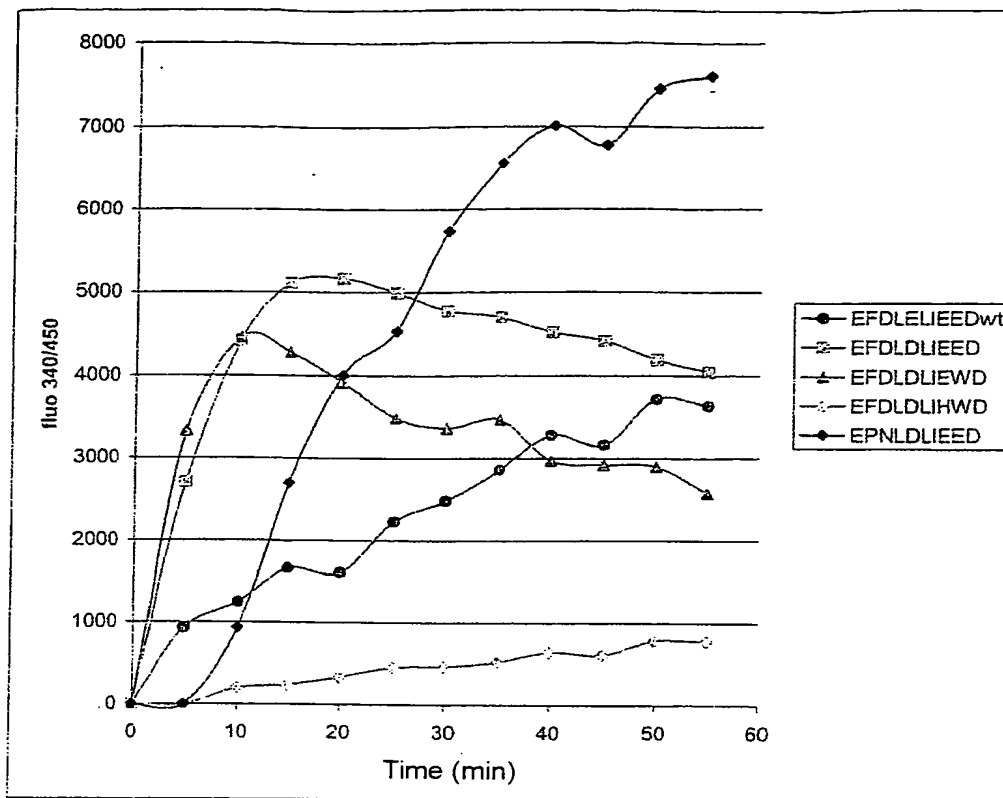


Figure 5